



## SEQUENCE LISTING

#6

&lt;110&gt;Medlock et al.

&lt;120&gt; IL-17 Receptor Like Molecules and Uses Thereof

&lt;130&gt; 01017/36917A

&lt;140&gt; US 09/810,927

&lt;141&gt; 2001-03-16

&lt;150&gt; US 60/266,159

&lt;151&gt; 2001-02-02

&lt;150&gt; US 09/723,232

&lt;151&gt; 2000-11-27

&lt;150&gt; US 60/204,208

&lt;151&gt; 2000-05-12

&lt;150&gt; US 60/189,923

&lt;151&gt; 2000-03-08

&lt;160&gt; 27

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1841

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)..(1555)

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Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn	
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Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu	
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Val Asn Phe Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile	
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Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser	
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Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly	
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Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu	
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 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
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 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr  
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 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val  
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 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu  
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 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr  
 225 230 235 240  
 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr  
 245 250 255  
 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro  
 260 265 270  
 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly  
 275 280 285  
 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val  
 290 295 300  
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 305 310 315 320  
 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val  
 325 330 335

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr  
 340 345 350  
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 420 425 430  
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 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro  
 450 455 460  
 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu  
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 50 55 60  
 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu  
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 85 90 95  
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala  
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 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg  
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Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Arg Trp Arg Thr  
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 Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val Ile Leu  
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 Ala Ile Ser Glu Ala Gly Val Met Thr Trp Val Gly Arg Gln Lys Gln  
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 Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro Val Arg  
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 55 60 65  
 gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298  
 Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala  
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 gtg agg ctg gag tgc agt ggt gcg atc atg gct cgc tgc gac ctc aat 394  
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act gca ggc gtg ggc cac cag acc tgg cta att ttt gta gtt ttt gta	490
Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val Val Phe Val	
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Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser Ala Gln Ala	
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Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln Trp Thr Phe	
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Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly	
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Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met	
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Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr	
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Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr	
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ccc ctg gga aac aga tac atg gct ctt atc caa cac agc act atc atc	874
Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile	
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Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu	
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Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly	
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 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
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 Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys  
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 Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly  
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 210 215 220  
 Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro  
 225 230 235 240  
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 245 250 255  
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 Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln  
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330

335

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 370 375 380  
 Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile  
 385 390 395 400  
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&lt;210&gt; 6

&lt;211&gt; 1713

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (273)..(1427)

&lt;400&gt; 6

ataaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcga tgtcgctcgt 60  
 gctgctaagc ctggccgcgc tgtgcaggag cgccgtaccc cgagagccga ccgttcaatg 120  
 tggctctgaa actgggccat ctccagagtg gatgctacaa catgatctaa tccccgggaga 180  
 cttgagggac ctccgagtag aacctgttac aactagtgtt gcaacagggg actattcaat 240

ttt	gat	gaat	gta	agc	tgg	tac	tcc	ggc	ag	atg	tgg	aca	ttt	tcc	tac	atc	293
										Met	Trp	Thr	Phe	Ser	Tyr	Ile	
										1				5			
ggc	ttc	cct	gta	gag	ctg	aac	aca	gtc	tat	ttc	att	ggg	gcc	cat	aat	341	
Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn		
		10					15					20					
att	cct	aat	gca	aat	atg	aat	gaa	gat	ggc	cct	tcc	atg	tct	gtg	aat	389	
Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn		
	25					30					35						
ttc	acc	tca	cca	ggc	tgc	cta	gac	cac	ata	atg	aaa	tat	aaa	aaa	aag	437	
Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys		
40					45					50					55		
tgt	gtc	aag	gcc	gga	agc	ctg	tgg	gat	ccg	aac	atc	act	gct	tgt	aag	485	
Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys		
				60					65					70			
aag	aat	gag	gag	aca	gta	gaa	gtg	aac	ttc	aca	acc	act	ccc	ctg	gga	533	
Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly		
			75				80						85				
aac	aga	tac	atg	gct	ctt	atc	caa	cac	agc	act	atc	atc	ggg	ttt	tct	581	
Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser		
		90					95					100					
cag	gtg	ttt	gag	cca	cac	cag	aag	aaa	caa	acg	cga	gct	tca	gtg	gtg	629	
Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val		
	105					110					115						
att	cca	gtg	act	ggg	gat	agt	gaa	ggc	gct	acg	gtg	cag	ctg	act	cca	677	
Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro		
120					125					130					135		
tat	ttt	cct	act	tgt	ggc	agc	gac	tgc	atc	cga	cat	aaa	gga	aca	gtt	725	
Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val		
				140					145					150			
gtg	ctc	tgc	cca	caa	aca	ggc	gtc	cct	ttc	cct	ctg	gat	aac	aac	aaa	773	
Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys		
			155					160					165				
agc	aag	ccg	gga	ggc	tgg	ctg	cct	ctc	ctc	ctg	ctg	tct	ctg	ctg	gtg	821	
Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val		
		170					175					180					
gcc	aca	tgg	gtg	ctg	gtg	gca	ggg	atc	tat	cta	atg	tgg	agg	cac	gaa	869	
Ala	Thr	Trp	Val	Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His	Glu		
	185					190											

tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc	1013
Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile	
235 240 245	
ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag	1061
Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln	
250 255 260	
tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt	1109
Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu	
265 270 275	
tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag	1157
Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu	
280 285 290 295	
ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac	1205
Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn	
300 305 310	
ctt ttc tgc agt gat cta aga agc cag att cat ctg cac aaa tac gtg	1253
Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val	
315 320 325	
gtg gtc tac ttt aga gag att gat aca aaa gac gat tac aat gct ctc	1301
Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu	
330 335 340	
agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt	1349
Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys	
345 350 355	
gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca	1397
Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser	
360 365 370 375	
caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccaccc atgagaagca	1447
Gln Ala Cys His Asp Gly Cys Cys Ser Leu	
380 385	
agagacctta aaggcttctt atcccaccaa ttacaggggaa aaaacgtgtg atgatacctga	1507
agcttactat gcagcctaca aacagcctta gtaattaa cttttatac caataaaatt	1567
ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc	1627
aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta accattttga	1687
taatgcaaca ataaagcatc ttcagc	1713
<210> 7	
<211> 385	
<212> PRT	
<213> Homo sapiens	
<400> 7	
Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val	
1 5 10 15	



Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp  
20 25 30  
Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His  
35 40 45  
Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp  
50 55 60  
Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn  
65 70 75 80  
Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His  
85 90 95  
Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys  
100 105 110  
Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly  
115 120 125  
Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys  
130 135 140  
Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro  
145 150 155 160  
Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu  
165 170 175  
Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile  
180 185 190  
Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr  
195 200 205  
Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu  
210 215 220  
Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn  
225 230 235 240  
His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile  
245 250 255  
Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala  
260 265 270  
Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp  
275 280 285  
Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp  
290 295 300  
Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln  
305 310 315 320  
Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr  
325 330 335  
Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met  
340 345 350

Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln  
355 360 365

Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser  
370 375 380

Leu  
385

<210> 8  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2429-59

<400> 8  
gcagacactg agagcattgt aatcg 25

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
1916-83

<400> 9  
ggctcgtatg ttgtgtggaa ttgtgag 27

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2429-56

<400> 10  
atcaagaaga cttccttttc tac 23

<210> 11  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer 1916-80

<400> 11  
tgcaaggcga ttaagttggg taacgccag 29

<210> 12  
<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 12  
gccgacgggg acgtggatga ac 22

<210> 13  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 13  
catgattacg ccaagctcta atacgactc 29

<210> 14  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 14  
cttcgccgag tgctgtgca g 21

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nest PCR  
Primer

<400> 15  
tcacgacgtt gtaaaacgac ggccagtg 28

<210> 16  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
2469-50

<400> 16  
gcgatgtcgc tcgtgctgct aag 23



<210> 17  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2469-54

<400> 17  
gcagcctggt gaggtgaaat tcac

24 ..

<210> 18  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 18  
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

<210> 19  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 19  
Phe Ile Thr Cys Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg  
1 5 10 15

Arg Arg

<210> 20  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Epogen signal  
peptide

<400> 20  
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu  
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly  
20 25

<210> 21  
<211> 233  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide of Fc  
fragment

<400> 21

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
1 5 10 15  
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
20 25 30  
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
35 40 45  
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
50 55 60  
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
65 70 75 80  
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
85 90 95  
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110  
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
115 120 125  
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
130 135 140  
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
145 150 155 160  
Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
165 170 175  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
180 185 190  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220  
Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 22

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (159)..(641)

<400> 22

ctcaagtcac tcctataaaa gacagtggaa ataaatttga ataaacaaaa caggcttgct 60

gaaaataaaa tcaggactcc taacctgctc cagtcagcct gcttccacga ggcctgtcag 120

tcagtgcgcc acttgtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176  
Met Tyr Gln Val Val Ala  
1 5

ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224  
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser  
10 15 20

tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272  
Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp  
25 30 35

agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320  
Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His  
40 45 50

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc 368  
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala  
55 60 65 70

atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc 416  
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro  
75 80 85

cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta 464  
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu  
90 95 100

cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac 512  
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr  
105 110 115

cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc 560  
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly  
120 125 130

acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta 608  
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu  
135 140 145 150

gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag 644  
Ala Cys Val Cys Val Arg Pro Arg Val Met Gly  
155 160

<210> 23  
<211> 161  
<212> PRT  
<213> Homo sapiens

<400> 23  
Met Tyr Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr His Thr  
1 5 10 15  
Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser  
20 25 30  
Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro  
35 40 45

Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly  
 50 55 60  
 Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg  
 65 70 75 80  
 Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys  
 85 90 95  
 Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly  
 100 105 110  
 Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro  
 115 120 125  
 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg  
 130 135 140  
 Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met  
 145 150 155 160  
 Gly

<210> 24  
 <211> 521  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
 1 5 10 15  
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
 20 25 30  
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
 35 40 45  
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 65 70 75 80  
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 85 90 95  
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser  
 100 105 110  
 Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn  
 115 120 125  
 Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn  
 130 135 140  
 Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu  
 145 150 155 160  
 Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu  
 165 170 175

Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu  
 180 185 190  
 Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile  
 195 200 205  
 Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln  
 210 215 220  
 Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser  
 225 230 235 240  
 Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser  
 245 250 255  
 Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly  
 260 265 270  
 Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu  
 275 280 285  
 Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 290 295 300  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 305 310 315 320  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 325 330 335  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 340 345 350  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 355 360 365  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 370 375 380  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 385 390 395 400  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 405 410 415  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 420 425 430  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 435 440 445  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 450 455 460  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 465 470 475 480  
 Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 485 490 495  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 500 505 510

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
515 520

<210> 25  
<211> 585  
<212> PRT  
<213> Homo sapiens

<400> 25  
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
1 5 10 15  
Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
20 25 30  
Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
35 40 45  
Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
50 55 60  
Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
65 70 75 80  
Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
85 90 95  
Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys  
100 105 110  
Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg  
115 120 125  
Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val  
130 135 140  
Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser  
145 150 155 160  
Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln  
165 170 175  
Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr  
180 185 190  
Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly  
195 200 205  
Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile  
210 215 220  
Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro  
225 230 235 240  
Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe  
245 250 255  
Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser  
260 265 270  
Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln  
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala  
 290 295 300  
 Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile  
 305 310 315 320  
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe  
 325 330 335  
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala  
 340 345 350  
 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 355 360 365  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 370 375 380  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 385 390 395 400  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 405 410 415  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 420 425 430  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 435 440 445  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 450 455 460  
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
 465 470 475 480  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
 485 490 495  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 500 505 510  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 515 520 525  
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 530 535 540  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 545 550 555 560  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 565 570 575  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 580 585

<210> 26  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

cattttccta catcggttc cctg

24

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 27

tgaatctggc ttctttcact gc

22